

Module	Main Category	Sub category of main category (if exist)	Description/Name	KGML	Paths	module_link	start_molecule	end_molecule
M00001	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Glycolysis (Embden-Meyerhof pathway), glucose => pyruvate	hsa000010	hsa01200;hsa00010 hsa01200;hsa01230;hsa00010	http://www.genome C00267: alpha-D-Glucose http://www.genome C00111: Glycerone phosphate	C00022: Pyruvate	
M00002	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Glycolysis, core module involving three-carbon compounds	hsa000010	hsa00010;hsa00020	http://www.genome C00036: Oxaloacetate	C00022: Pyruvate	
M00003	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Gluconeogenesis, oxaloacetate => fructose-6P	hsa000010	hsa00010;hsa00020	http://www.genome C01172: beta-D-Glucose 6-phosphate	C05345: beta-D-Fructose 6-phosphate	
M00004	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Pentose phosphate pathway (Pentose phosphate cycle)	hsa000030	hsa01200;hsa00030	http://www.genome C01172: beta-D-Glucose 6-phosphate	C01172: beta-D-Glucose 6-phosphate	
M00006	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Pentose phosphate pathway, oxidative phase, glucose 6P => ribulose 5P	hsa000030	hsa01200;hsa00030	http://www.genome C01172: beta-D-Glucose 6-phosphate	C00199: D-Ribulose 5-phosphate	
M00007	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Pentose phosphate pathway, non-oxidative phase, fructose 6P => ribose	hsa000030	hsa01200;hsa01230;hsa00030	http://www.genome C05345+C00118: beta-D-Fructose 6-phosphate + D-Glyceraldehyde 3-phosq	C00117: D-Ribose 5-phosphate	
M00009	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Citrate cycle (TCA cycle, Krebs cycle)	hsa000020	hsa01200;hsa00020	http://www.genome C00024+C00036: Acetyl-CoA + Oxaloacetate	C00036: Oxaloacetate	
M00010	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Citrate cycle, first carbon oxidation, oxaloacetate => 2-oxoglutarate	hsa000020	hsa01200;hsa01210;hsa01230;hsa00020	http://www.genome C00036+C00024: Oxaloacetate + Acetyl-CoA	C00026: 2-Oxoglutarate	
M00011	Carbohydrate and lipid metabolism	Central carbohydrate metabolism	Citrate cycle, second carbon oxidation, 2-oxoglutarate => oxaloacetate	hsa000020	hsa01200;hsa00020	http://www.genome C00026+C15972: 2-Oxoglutarate + Enzyme N6-(lipoyl)lysine	C00036: Oxaloacetate	
M00013	Carbohydrate and lipid metabolism	Other carbohydrate metabolism	Malonate semialdehyde pathway, propanoyl-CoA => acetyl-CoA	hsa000640	hsa01200;hsa00640	http://www.genome C00100: Propanoyl-CoA	C00024: Acetyl-CoA	
M00014	Carbohydrate and lipid metabolism	Other carbohydrate metabolism	Glucuronate pathway (uronate pathway)	hsa000040	hsa00040	http://www.genome C00029: UDP-glucose	C00231: D-Xylose 5-phosphate	
M00015	Nucleotide and amino acid metabolism	Arginine and proline metabolism	Proline biosynthesis, glutamate => proline	hsa000330	hsa01230;hsa00330	http://www.genome C00025: L-Glutamate	C00148: L-Proline	
M00020	Nucleotide and amino acid metabolism	Serine and threonine metabolism	Serine biosynthesis, glycerate-3P => serine	hsa000260	hsa01200;hsa01230;hsa00260	http://www.genome C00197: 3-Phospho-D-glycerate	C00065: L-Serine	
M00027	Nucleotide and amino acid metabolism	Other amino acid metabolism	GABA (gamma-Aminobutyrate) shunt	hsa000250	hsa00250	http://www.genome C00025: L-Glutamate	C00042: Succinate	
M00029_1	Nucleotide and amino acid metabolism	Arginine and proline metabolism	Urea cycle	hsa00220	hsa01230;hsa00220	http://www.genome C00014+C00049: Ammonia + L-Aspartate	C00122: Fumarate	
M00029_2	Nucleotide and amino acid metabolism	Arginine and proline metabolism	Urea cycle	hsa00220	hsa01230;hsa00220	http://www.genome C00014+C00049: Ammonia + L-Aspartate	C00086: Urea	
M00032	Nucleotide and amino acid metabolism	Lysine metabolism	Lysine degradation, lysine => saccharopine => acetoacetyl-CoA	hsa00310	hsa00310	http://www.genome C00047: L-Lysine	C00332: Acetoacetyl-CoA	
M00034_1	Nucleotide and amino acid metabolism	Cysteine and methionine metabolism	Methionine salvage pathway	hsa00270	hsa00270	http://www.genome C00073: L-Methionine	C00147: Adenine	
M00035_1	Nucleotide and amino acid metabolism	Cysteine and methionine metabolism	Methionine degradation	hsa00270	hsa00270	http://www.genome C00073+C00065: L-Methionine + L-Serine	C02291: L-Cystathione	
M00036	Nucleotide and amino acid metabolism	Branched-chain amino acid metabolism	Leucine degradation, leucine => acetoacetate + acetyl-CoA	hsa00280	hsa00280	http://www.genome C00123: L-Leucine	C00164: Acetoacetate	
M00037	Nucleotide and amino acid metabolism	Aromatic amino acid metabolism	Melatonin biosynthesis, tryptophan => serotonin => melatonin	hsa00380	hsa00380	http://www.genome C00078: L-Tryptophan	C01598: Melatonin	
M00042	Nucleotide and amino acid metabolism	Aromatic amino acid metabolism	Catecholamine biosynthesis, tyrosine => dopamine => noreadrenaline =>	hsa00350	hsa00350	http://www.genome C00082: L-Tyrosine	C00788: L-Adrenaline	
M00043	Nucleotide and amino acid metabolism	Aromatic amino acid metabolism	Thyroid hormone biosynthesis, tyrosine => triiodothyronine/thyroxine	hsa00350	hsa00350	http://www.genome C00082: L-Tyrosine	C02465: Triiodothyronine	
M00044_1	Nucleotide and amino acid metabolism	Aromatic amino acid metabolism	Tyrosine degradation, tyrosine => homogenisate	hsa00350	hsa00350	http://www.genome C00122: Fumarate	C00122: Fumarate	
M00046_1	Nucleotide and amino acid metabolism	Pyrimidine metabolism	Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutene	hsa00240	hsa00240	http://www.genome C00106: Uracil	C00099: beta-Alanine	
M00046_2	Nucleotide and amino acid metabolism	Pyrimidine metabolism	Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutene	hsa00240	hsa00240	http://www.genome C00178: Thymine	C05145: 3-Aminoisobutyric acid	
M00047	Nucleotide and amino acid metabolism	Other amino acid metabolism	Creatine pathway	hsa00330	hsa00330	http://www.genome C00062: L-Arginine	C00791: Creatinine	
M00048	Nucleotide and amino acid metabolism	Purine metabolism	Inosine monophosphate biosynthesis, PRPP + glutamine => IMP	hsa00230	hsa00230	http://www.genome C00119+C00064: 5-Phospho-alpha-D-ribose 1-diphosphate + L-Glutamine	C00130: IMP	
M00049	Nucleotide and amino acid metabolism	Purine metabolism	Adenine ribonucleotide biosynthesis, IMP => ADP,ATP	hsa00230	hsa00230	http://www.genome C00130: IMP	C00002: ATP	
M00050	Nucleotide and amino acid metabolism	Purine metabolism	Guanine ribonucleotide biosynthesis IMP => GDP,GTP	hsa00230	hsa00230	http://www.genome C00130: IMP	C00044: GTP	
M00051_1	Nucleotide and amino acid metabolism	Pyrimidine metabolism	Uridine monophosphate biosynthesis, glutamine (+ PRPP) => UMP	hsa00240	hsa00240	http://www.genome C00064+C00119: L-Glutamine + 5-Phospho-alpha-D-ribose 1-diphosphate	C00105: UMP	
M00052	Nucleotide and amino acid metabolism	Pyrimidine metabolism	Pyrimidine ribonucleotide biosynthesis, UMP => UDP/UTP,CDP/CTP	hsa00240	hsa00240	http://www.genome C00105: UMP	C00112: CDP	
M00055	Carbohydrate and lipid metabolism	Glycan metabolism	N-glycan precursor biosynthesis	hsa00510	hsa00510	http://www.genome C00110: Dolichyl phosphate	G00008:	
M00056_1	Carbohydrate and lipid metabolism	Glycan metabolism	O-glycan biosynthesis, mucin type core	hsa00512	hsa00512	http://www.genome C02189+G10611: [Protein]-L-serine	G00025:	
M00056_2	Carbohydrate and lipid metabolism	Glycan metabolism	C-glycan biosynthesis, mucin type core	hsa00512	hsa00512	http://www.genome C02189+G10611: [Protein]-L-serine	G00029:	
M00056_3	Carbohydrate and lipid metabolism	Glycan metabolism	C-glycan biosynthesis, mucin type core	hsa00512	hsa00512	http://www.genome C02189+G10611: [Protein]-L-serine	G00031:	
M00057	Carbohydrate and lipid metabolism	Glycosaminoglycan metabolism	Glycosaminoglycan biosynthesis, linkage tetrasaccharide	hsa00532	hsa00532	http://www.genome C02189: [Protein]-L-serine	G00157:	
M00058	Carbohydrate and lipid metabolism	Glycosaminoglycan metabolism	Glycosaminoglycan biosynthesis, chondroitin sulfate backbone	hsa00532	hsa00532	http://www.genome G00157:	G00160:	
M00059	Carbohydrate and lipid metabolism	Glycosaminoglycan metabolism	Glycosaminoglycan biosynthesis, heparan sulfate backbone	hsa00534	hsa00534	http://www.genome G00157:	G00164:	
M00065	Carbohydrate and lipid metabolism	Glycan metabolism	GPI-anchor biosynthesis, core oligosaccharide	hsa00563	hsa00563	http://www.genome C0194: 1-Phosphatidyl-D-myo-inositol	G13044:	
M00066	Carbohydrate and lipid metabolism	Lipid metabolism	Lactosylceramide biosynthesis	hsa00600	hsa00600	http://www.genome C00195: N-Acylsphingosine	C01290: beta-D-Galactosyl-(1->4)-beta-D-glucosyl-(11)-c	
M00067_1	Carbohydrate and lipid metabolism	Lipid metabolism	Cerebroside and sulfatide biosynthesis	hsa00600	hsa00600;hsa00565	http://www.genome C00195: N-Acylsphingosine	C06125: Sulfatide	
M00067_2	Carbohydrate and lipid metabolism	Lipid metabolism	Cerebroside and sulfatide biosynthesis	hsa00600	hsa00600;hsa00565	http://www.genome C0201: 1-Alkyl-2-acylglycerol	C20825: Seminolipid	
M00068	Carbohydrate and lipid metabolism	Glycan metabolism	Glycosphingolipid biosynthesis, globo-series, LacCer => Gb4Cer	hsa00603	hsa00603	http://www.genome G00092:	G00094:	
M00069	Carbohydrate and lipid metabolism	Glycan metabolism	Glycosphingolipid biosynthesis, ganglio series, LacCer => GT3	hsa00604	hsa00604	http://www.genome G00092:	G00118:	
M00070	Carbohydrate and lipid metabolism	Glycan metabolism	Glycosphingolipid biosynthesis, lacto-series, LacCer => Lc4Cer	hsa00601	hsa00601	http://www.genome G00092:	G00037:	
M00071	Carbohydrate and lipid metabolism	Glycan metabolism	Glycosphingolipid biosynthesis, neolacto-series, LacCer => nLc4Cer	hsa00601	hsa00601	http://www.genome G00092:	G00050:	
M00073	Carbohydrate and lipid metabolism	Glycan metabolism	N-glycan precursor trimming	hsa00510	hsa00510	http://www.genome G00009:	G00012:	
M00075_1	Carbohydrate and lipid metabolism	Glycan metabolism	N-glycan biosynthesis, complex type	hsa00510	hsa00510	http://www.genome G00013:	G00019:	
M00075_2	Carbohydrate and lipid metabolism	Glycan metabolism	N-glycan biosynthesis, complex type	hsa00510	hsa00510	http://www.genome G00013:	G00022:	
M00075_3	Carbohydrate and lipid metabolism	Glycan metabolism	N-glycan biosynthesis, complex type	hsa00510	hsa00510	http://www.genome G00013:	G00018:	
M00076	Carbohydrate and lipid metabolism	Glycosaminoglycan metabolism	Dermatan sulfate degradation	hsa00531	hsa00531	http://www.genome C00426: Dermatan sulfate	G00872:	
M00077	Carbohydrate and lipid metabolism	Glycosaminoglycan metabolism	Chondroitin sulfate degradation	hsa00531	hsa00531	http://www.genome G12336:	G00872:	
M00078	Carbohydrate and lipid metabolism	Glycosaminoglycan metabolism	Heparan sulfate degradation	hsa00531	hsa00531	http://www.genome C00925: Heparan sulfate	G02632:	
M00079	Carbohydrate and lipid metabolism	Glycosaminoglycan metabolism	Keratan sulfate degradation	hsa00531	hsa00531	http://www.genome C00573: Keratan sulfate	G01391:	
M00082	Carbohydrate and lipid metabolism	Fatty acid metabolism	Fatty acid biosynthesis, initiation	hsa00061	hsa01212;hsa00061	http://www.genome C00024: Acetyl-CoA	C05744: Acetoacetyl-[acp]	
M00083	Carbohydrate and lipid metabolism	Fatty acid metabolism	Fatty acid biosynthesis, elongation	hsa00061				

M00135	Nucleotide and amino acid metabolism	Polyamine biosynthesis	GABA biosynthesis, eukaryotes, putrescine => GABA	hsa00330	http://www.genome.jp/kegg-bin/get_htext	C00334: 4-Aminobutanoate
M00141	Nucleotide and amino acid metabolism	Cofactor and vitamin biosynthesis	C1-unit interconversion, eukaryotes	hsa00670	http://www.genome.jp/kegg-bin/get_htext	C00101: Tetrahydrofolate
M00338_1	Nucleotide and amino acid metabolism	Cysteine and methionine metabolism	Cysteine biosynthesis, homocysteine + serine => cysteine	hsa00270	http://www.genome.jp/kegg-bin/get_htext	C00097: L-Cysteine
M00367	Nucleotide and amino acid metabolism	Terpenoid backbone biosynthesis	C10-C20 isoprenoid biosynthesis, non-plant eukaryotes	hsa00900	http://www.genome.jp/kegg-bin/get_htext	C00353: Geranylgeranyl diphosphate
M00415	Nucleotide and amino acid metabolism	Fatty acid metabolism	Fatty acid biosynthesis, elongation, endoplasmic reticulum	hsa00062	http://www.genome.jp/kegg-bin/get_htext	C20876: Very-long-chain acyl-CoA
M00549	Carbohydrate and lipid metabolism	Other carbohydrate metabolism	Nucleotide sugar biosynthesis, glucose => UDP-glucose	hsa00520	http://www.genome.jp/kegg-bin/get_htext	C00029: UDP-glucose
M00554	Carbohydrate and lipid metabolism	Other carbohydrate metabolism	Nucleotide sugar biosynthesis, galactose => UDP-galactose	hsa00520;hsa00052	http://www.genome.jp/kegg-bin/get_htext	C00052: UDP-alpha-D-galactose
M00632_1	Carbohydrate and lipid metabolism	Other carbohydrate metabolism	Galactose degradation, Leloir pathway, galactose => alpha-D-glucose-1F	hsa00052	http://www.genome.jp/kegg-bin/get_htext	C00103: D-Glucose 1-phosphate
M00741	Carbohydrate and lipid metabolism	Other carbohydrate metabolism	Propanoyl-CoA metabolism, propanoyl-CoA => succinyl-CoA	hsa00280	http://www.genome.jp/kegg-bin/get_htext	C00091: Succinyl-CoA

*http://www.genome.jp/kegg-bin/get_htext

Aldosterone (M00108_C01780)	Down (3.17e-12)	Down (1.16e-14)	Up (4.04e-07)	
Cortisone (M00109_C00762)	Down (0.00994)	Down (0.00497)	Down (1.16e-12)	Down (0.00749) Down (0.0128)
Estrone (M00110_C00468)		Up (3.63e-06)	Up (0.0152)	Down (0.0186)
Glutathione (M00118_C00051)		Down (0.00139)		Up (6.62e-07)
CoA (M00120_C00010)	Up (9.74e-31)		Down (1.74e-16)	Up (1.77e-07)
Ubiquinone (M00128_C00399)	Up (1.31e-09)	Down (1.33e-10)	Down (3.99e-25)	Down (4.35e-05)
1D-myoinositol 1,3,4,5-tetrakisphosphate (M00130_C01272)	Down (5.43e-42)	Up (1.39e-14)	Down (3.5e-10)	Unknown (0.0233)
myo-Inositol (M00131_C00137)	Up (0.000437)	Down (0.0223)	Up (2.21e-12)	Unknown (0.0233)
Phytic acid (M00132_C01204)		Down (0.000525)		Unknown (0.0233)
Spermidine (M00133_C00315)		Up (0.0315)	Up (7.28e-19)	Up (2.94e-13)
Putrescine (M00134_C00134)	Down (9.62e-16)	Down (0.000205)	Down (8.28e-29)	
4-Aminobutanate (M00135_C00334)	Down (3.91e-42)	Down (3.35e-16)	Down (2.27e-07)	Down (0.0138)
C1-unit interconversion (M00141)	Up (0.0167)	Down (2.63e-17)	Down (0.00222)	Up (3.03e-14)
L-Cysteine (M00338_C00097)	Up (2.11e-09)	Down (7.38e-16)	Down (3.48e-29)	Up (9.44e-11)
Geranylgeranyl diphosphate (M00367_C00353)	Up (1.22e-40)	Up (2.88e-11)	Down (1.18e-10)	Up (0.000693)
Very-long-chain acyl-CoA (M00415_C20876)	Up (1.27e-61)	Up (1.49e-26)	Up (1.06e-40)	Up (1.62e-28)
UDP-glucose (M00549_C00029)	Down (7.92e-31)	Down (1.23e-05)	Up (6.14e-14)	Down (9.92e-08)
UDP-alpha-D-galactose (M00554_C00052)			Down (0.00149)	
D-Glucose 1-phosphate (M00632_C00103)	Up (0.0346)	Down (0.000985)	Down (6.04e-10)	
Succinyl-CoA (M00741_C00091)		Down (2.14e-20)	Down (1.21e-33)	Unknown (1.26e-05) Up (0.000249)



Metabolite



Reaction node



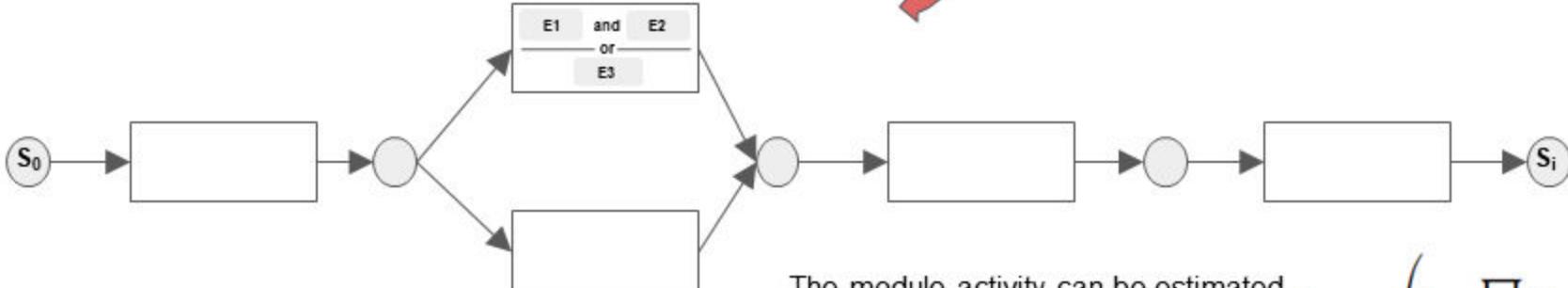
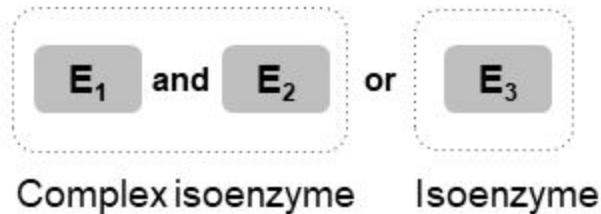
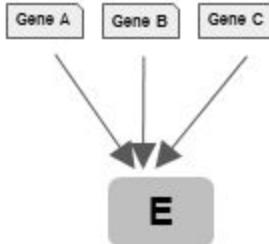
Isoenzyme



Enzyme



Gene



3 The module activity can be estimated from the reaction node activities using the equation:

$$S_i = n_i \cdot \left(1 - \prod_{s_a \in A_i} (1 - s_a) \right)$$

